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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=1; day=18; hr=17; min=20; sec=53; ms=127;]

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Reviewer Comments:

<210> SEQ ID NO 1

<211> LENGTH: 35

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Primer

Please remove all line headers from the sequence listing, i.e. SEQ ID NO, LENGTH:, TYPE: ...etc.

Application No: 10500240

Version No: 2.0

Input Set:**Output Set:****Started:** 2007-12-28 12:28:19.445**Finished:** 2007-12-28 12:28:24.889**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 444 ms**Total Warnings:** 23**Total Errors:** 31**No. of SeqIDs Defined:** 106**Actual SeqID Count:** 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-12-28 12:28:19.445
Finished: 2007-12-28 12:28:24.889
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 444 ms
Total Warnings: 23
Total Errors: 31
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (54)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
E 257	Invalid sequence data feature in <221> in SEQ ID (62)
E 257	Invalid sequence data feature in <221> in SEQ ID (68)
E 257	Invalid sequence data feature in <221> in SEQ ID (70)
E 257	Invalid sequence data feature in <221> in SEQ ID (72)
E 257	Invalid sequence data feature in <221> in SEQ ID (78)
	This error has occurred more than 20 times, will not be displayed

<110> APPLICANT: GLYCOFI, INC.
 <120> TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE
 STRUCTURES
 <130> FILE REFERENCE: GFI/102 PCT

 <140> CURRENT APPLICATION NUMBER:10500240
 <141> CURRENT FILING DATE:2005-03-23
 <150> PRIOR APPLICATION NUMBER: 60/344,169
 <151> PRIOR FILING DATE: 2001-12-27
 <160> NUMBER OF SEQ ID NOS: 106
 <170> SOFTWARE: PatentIn Ver. 2.1

 <210> SEQ ID NO 1
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 1
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 2
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 <210> SEQ ID NO 3
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 3
 cctaagctgg tatgcgttct ctttgccata tc 32

 <210> SEQ ID NO 4
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 <210> SEQ ID NO 5
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 gtaatacgcac tcactatagg gc 22

<210> SEQ ID NO 7
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 ccacatcatc cgtgctacat atag 24

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<210> SEQ ID NO 9
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<210> SEQ ID NO 10
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 agcctcagcg ccaacaagcg atgg 24

<210> SEQ ID NO 11
 <211> LENGTH: 44
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 ctggataacc ctcgatactt cgagatctgt ttagcttgcc tcgt 44

<210> SEQ ID NO 12
 <211> LENGTH: 44
 <212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<210> SEQ ID NO 13
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
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 atcctttacc gatgctgtat 20

<210> SEQ ID NO 14
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<210> SEQ ID NO 15
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 <212> TYPE: DNA
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 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<210> SEQ ID NO 16
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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<210> SEQ ID NO 17
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 aatgagatga ggctccgcaa tggaactg 28

<210> SEQ ID NO 18
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

<400> SEQUENCE: 18
 ctgattgctt atcaacgaga attccttg 28

<210> SEQ ID NO 19
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 19
 tgttgggttc tcagatgatc agttgggtg 28

<210> SEQ ID NO 20
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 20
 agagagagat ggctttcttt tctccctgg 29

<210> SEQ ID NO 21
 <211> LENGTH: 27
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 21
 aaatcaagtg gatgaaggac atgtggc 27

<210> SEQ ID NO 22
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 22
 agcgatgcta taggcagtct ttgcagag 28

<210> SEQ ID NO 23
 <211> LENGTH: 4
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces cerevisiae
 <400> SEQUENCE: 23
 His Asp Glu Leu
 1

<210> SEQ ID NO 24
 <211> LENGTH: 458
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces cerevisiae
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (304)..(318)
 <223> OTHER INFORMATION: Variable amino acid
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES

<222> LOCATION: (416)..(436)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 24

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys
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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
			35				40					45			
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
			50				55					60			
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
					70					75					80
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
				85					90					95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
			100					105						110	
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
			115				120					125			
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
			130			135					140				
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
145					150					155					160
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
				165				170					175		
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
			180					185					190		
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
			195				200					205			
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
			210			215					220				
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
225					230					235				240	
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
				245					250					255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
			260					265					270		
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
			275				280					285			
Asn	Trp	Gln	Met	Met	Asp	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	
			290			295				300					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Val
305					310					315				320	
Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
				325					330					335	
Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile
			340					345					350		
Pro	Phe	Val	Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg
			355				360					365			
Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile
			370			375					380				
Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr
385					390					395				400	
Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420				425					430			

Xaa	Xaa	Xaa	Xaa	Ser	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ser	His	Leu	Arg
	435						440					445			
Thr	Thr	Ser	Ser	Met	Glu	Lys	Lys	Leu	Asn						
	450						455								

<210> SEQ ID NO 25

<211> LENGTH: 458

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 25

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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
			35				40						45		
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
			50				55				60				
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
					70					75					80
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
					85					90				95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
			100					105						110	
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
			115				120					125			
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
			130				135					140			
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
					150					155					160
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
					165					170				175	
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
			180					185						190	
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
			195				200					205			
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
			210				215					220			
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
					230					235					240
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
					245					250				255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
			260					265						270	
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
			275					280					285		
Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	His
			290				295					300			
Leu	Ala	Leu	Leu	Ile	Ser	His	Leu	Ile	Ala	Leu	Thr	Thr	Leu	Phe	Val
					310					315				320	
Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
					325					330				335	
Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile
			340						345				350		
Pro	Phe	Val	Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg
			355					360					365		
Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile

370	375	380
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		
385	390	395
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala		400
	405	410
Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Ala		415
	420	425
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		430
	435	440
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn		445
450	455	

<210> SEQ ID NO 26

<211> LENGTH: 443

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (333)..(347)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 26

Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg		
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Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu		
	20	25
Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys		30
	35	40
Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp		45
	50	55
Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly		60
	65	70
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp		75
	85	90
His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr		95
	100	105
Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp		110
	115	120
Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val		125
	130	135
Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr		140
	145	150
Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu		155
	165	170
Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met		175
	180	185
Cys Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe		190
	195	200
Asn Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu		205
	210	215
Leu Ala Gln Arg Trp Gly Trp Gly Ser Leu Ala Leu Val Ile Ser Ala		220
	225	230
Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe		235
	245	250
Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile		255
	260	265
Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val		270
	275	280
		285

Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu	His	Cys	Ala
290						295					300				
Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile	Asn	Trp	Gln
305					310					315					320
Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa	Xaa	Xaa	Xaa
			325						330					335	